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Sequence Listing was accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=7; day=28; hr=15; min=36; sec=51; ms=272;]

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Application No: 10824481

Version No: 3.0

Input Set:

Output Set:

Started: 2008-07-25 21:57:31.911

Finished: 2008-07-25 21:57:34.026

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 115 ms

Total Warnings: 25

Total Errors: 0

No. of SeqIDs Defined: 35

Actual SeqID Count: 35

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
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W 213	Artificial or Unknown found in <213> in SEQ ID (29)
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Input Set:

Output Set:

Started: 2008-07-25 21:57:31.911
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Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 115 ms
Total Warnings: 25
Total Errors: 0
No. of SeqIDs Defined: 35
Actual SeqID Count: 35

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Wyeth
Ling, Vincent
Carreno, Beatriz M.
Collins, Mary

<120> USE OF B7-H3 TO INHIBIT LYMPHOCYTE PROLIFERATION (As Amended)

<130> 08702.6108-00000

<140> 10824481

<141> 2004-04-15

<160> 35

<170> PatentIn version 3.5

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<211> 951

<212> DNA

<213> Homo sapiens

<400> 1

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cctatgacat tccccccaga ggccctgtgg gtgaccgtgg ggctgtctgt ctgtctcatt	780
gcactgctgg tggccctggc ttctgtgtgc tggagaaaga tcaaacagag ctgtgaggag	840
gagaatgcag gagctgagga ccaggatggg gagggagaag gctccaagac agccctgcag	900
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<212> PRT
<213> Homo sapiens

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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu

195

200

205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
 210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln
 225 230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser
 245 250 255

Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg
 260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln
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 ctggtggaca cggatgccac cctacgtgc tccttttccc cagagcctgg cttcagttctg 180
 gcacagctca acctcatctg gcagctgaca gacaccaaac agctggtgca cagcttcacg 240
 gaggggccggg accaaggcag tgcctactcc aaccgcacag cgctcttccc tgacctgttg 300
 gtgcaaggca atgcgtcctt gaggtgtcag cgcgtccgag taaccgacga gggcagctac 360
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 ccctactcga agcccagcat gaccctggag cccaacaagg acctacgtcc agggaaacatg 480
 gtgaccatca cgtgctctag ctaccagggc tatccggagg ccgaggtgtt ctggaaggat 540
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ttgttcgatg ttcacagcgt gctgaggggtg gtgctgggtg ctaacggcac ctacagctgc	660
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gagaatgcag gtgccgagga ccaggatgga gatggagaag gatccaagac agctctacgg	900
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Val	Ser	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Asp	Thr	Asp	Ala	Thr	Leu
		35						40				45			

Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn
	50					55					60				

Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Thr
65					70				75						80

Glu	Gly	Arg	Asp	Gln	Gly	Ser	Ala	Tyr	Ser	Asn	Arg	Thr	Ala	Leu	Phe
				85					90					95	

Pro	Asp	Leu	Leu	Val	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val
		100						105					110		

Arg	Val	Thr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Phe	Val	Ser	Ile	Gln	Asp
		115					120					125			

Phe	Asp	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys
	130					135						140			

Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asn	Met
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
165 170 175

Phe Trp Lys Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr
180 185 190

Ser Gln Met Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn
210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln
225 230 235 240

Pro Leu Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser
245 250 255

Val Cys Leu Val Val Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg
260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln
275 280 285

Asp Gly Asp Gly Glu Gly Ser Lys Thr Ala Leu Arg Pro Leu Lys Pro
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Ser Glu Asn Lys Glu Asp Asp Gly Gln Glu Ile Ala
305 310 315

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ctggtgggca cogatgccac cctgtgctgc tccttctccc ctgagcctgg cttcagcctg 180
gcacagctca acctcatctg gcagctgaca gataccaaac agctgggtgca cagctttgct 240

Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly Ala
1 5 10 15

Ala	Leu	Gly	Ala	Leu	Trp	Phe	Cys	Leu	Thr	Gly	Ala	Leu	Glu	Val	Gln	20	25	30
Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	Ala	Thr	Leu	35	40	45
Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn	50	55	60
Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Ala	65	70	75
Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn	Arg	Thr	Ala	Leu	Phe	85	90	95
Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val	100	105	110
Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	115	120	125
Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	130	135	140
Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	145	150	155
Val	Thr	Ile	Thr	Cys	Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	165	170	175
Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	180	185	190
Ser	Gln	Met	Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Ile	Leu	195	200	205
Arg	Val	Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	210	215	220
Pro	Val	Leu	Gln	Gln	Asp	Ala	His	Ser	Ser	Val	Thr	Ile	Thr	Pro	Gln	225	230	235
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Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val
245 250 255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro
260 265 270

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr
275 280 285

Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly
290 295 300

Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln
305 310 315 320

Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
325 330 335

Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
340 345 350

Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
355 360 365

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
370 375 380

Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
385 390 395 400

Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu
405 410 415

Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala
420 425 430

Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp
435 440 445

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro
450 455 460

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu

465 470 475 480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys
485 490 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly
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Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp
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Asp Gly Gln Glu Ile Ala
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<212> PRT
<213> Homo sapiens

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35 40 45

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn
50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu
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<213> Homo sapiens

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20 25 30

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35 40 45

Val His Ser Phe Xaa Glu Gly Xaa Asp Gln Gly Ser Ala Tyr Ala Asn
50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu
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